

GenCore version 5.1.4\_p5-4578  
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2003, 23:36:55 ; Search time 2268 seconds  
(without alignments)

12339.418 Million cell updates/sec

Title: US-09-847-081b-1

Perfect score: 1728  
Sequence: 1 agaaaccagaagaacaac.....tcatcaaacctcaagtga 1728

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_estc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_est3:\*

12: gb\_est4:\*

13: gb\_est5:\*

14: gb\_est6:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pin:\*

21: em\_gss\_vit:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rdo:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	655.4	37.9	781	14	BQ511016
2	621.6	36.0	751	14	BQ046203
3	605.2	35.0	787	13	BM410846
4	568.4	32.9	677	12	BG351357
5	552.2	32.0	686	10	AW442101
6	551.2	31.9	785	13	BM408984

7	541.2	31.3	682	13	BM409200
8	532.8	30.8	672	10	AW442407
9	522	30.2	642	10	BE433198
10	515.8	29.8	676	10	AW222027
11	498.2	28.8	634	13	BM412533
12	487.2	28.2	599	13	BI921390
13	486.4	28.1	600	10	BE460889
14	483.4	28.0	623	10	BE432511
15	478.8	27.7	685	10	AW221932
16	473.2	27.4	582	10	AW223316
17	466.8	27.0	582	10	AW223666
18	466.4	27.0	581	10	BE432955
19	466.4	27.0	623	13	BM536249
20	461	26.7	791	10	AW223528
21	458.4	26.5	573	10	BE435308
22	458.4	26.5	605	10	BE435064
23	458.2	26.5	585	10	AW222245
24	458	26.5	1655	11	AY111032
25	457.8	26.5	585	10	BE432595
26	453.2	26.2	562	10	BE433966
27	449.4	26.0	581	10	AW222806
28	442.4	25.6	556	10	AW222152
29	439.6	25.4	542	10	BE431550
30	439	25.4	543	13	BM411875
31	437.4	25.3	634	10	AW441216
32	435	25.2	555	10	BE460463
33	434.4	25.1	566	12	BF112979
34	431.6	25.0	542	10	BE432748
35	429.2	24.8	563	10	BE461396
36	427.8	24.8	580	10	AW092690
37	427.6	24.7	563	10	BE437095
38	426.8	24.7	536	10	BE434911
39	425.4	24.6	558	10	AW222427
40	425.4	24.6	1201	11	AY108547
41	424.2	24.5	744	13	BM412719
42	423.6	24.5	551	10	BE432084
43	415.2	24.0	536	10	AW223238
44	409.2	23.7	519	10	BE433537
45	405.2	23.4	717	10	AW223529

## ALIGNMENTS

RESULT 1  
BQ511016/c  
LOCUS  
DEFINITION  
BQ511016  
BQ511016.2  
GI:21926690  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

781 bp mRNA linear EST 22-JUL-2002  
Generation of a set of potato cDNA clones for microarray  
analyses mixed potato tissues Solanum tuberosum cDNA clone STM067  
3' end, mRNA sequence.

potato.

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 781)

Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,

Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J., and

Karamycheva, S.A.

Generation of a set of potato cDNA clones for microarray analyses

Unpublished (2002)

On Jun 10, 2002 this sequence version replaced gi:21369885.

Other ESTs: EST618430

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Email: potato@igr.org

This clone is available through the Research Genetics, contact the

Research Genetics for further information 1-800-711-6195 or

cdna@resgen.com





Db 782 GAAGG 787

RESULT 4  
BG351357  
LOCUS 10412 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA EST 01-MAR-2001  
DEFINITION sequence.  
ACCESSION BG351357  
VERSION BG351357.1 GI:13180099  
KEYWORDS EST.  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanales; Solanaceae; Solanum.  
REFERENCE 1 (bases 1 to 677)  
AUTHORS Nielsen, K.L., Crookshanks, M., Emmersen, J. and Welinder, K.G.  
TITLE EST-sequencing of mature potato tuber (Var. Kuras)  
JOURNAL Unpublished (2000)  
COMMENT Contact: Karen G. Welinder  
Institut for bioteknologi  
Aalborg Universitet  
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark  
Tel: +45 96358467  
Fax: +45 98141808  
Email: kwebio.auc.dk  
Sequenced from the 5' end.  
High quality sequence stop: 677  
POLYA-No.

FEATURES  
source  
1..677  
/organism="Solanum tuberosum"  
/cultivar="Field grown Kuras"  
/db\_xref="taxon:4113"  
/clone\_lib="Mature tuber lambda ZAP"  
/tissue\_type="Tuber"  
/note="Vector: Lambda ZAP"  
BASE COUNT 192 a 102 c 198 g 185 t  
ORIGIN

Query Match 32.9%; Score 568.4; DB 12; Length 677;  
Best Local Similarity 90.9%; Pred. No. 2e-148;  
Matches 616; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 316 GATTCAGTCCGAGAGGAAACCGCGTCTTTCTATCATCCAGGTTCCAGTCCGAGATAGG 375  
Db 1 GATTCAGTCCGAGAGGAAACCGCGTCTTTCTATCATCCAGGTTCCAGTCCGAGATAGG 59

QY 376 AATTGTGTGGAATGGAATCAAGAAAGGTGGGAGACAAAGGTGGAATTTTGGCTCT 435  
Db 60 AATTCGATGTGGAAGGGAGATTCAGAAAGGTGGGAGACAGAGTGGAAATTTGGGTTT 119

QY 436 TTAATGCTGTATCAAGATATTCATGCTTGGGTGGATCAAGAATCAAGAGGAGCACT 495  
Db 120 TTAATGCGATTTGAGATATTCGTTGTTAGGAAGATCAAGAATCAAGAGGAGT 179

QY 496 TTCTCTGTACAGTCCAGTTGGTGGCTAGCCAGTCCGAGAAAGTCTGTCATCAGAG 555  
Db 180 TTTCTGTACAGTCCAGTTGGTGGCTAGCCAGTCCGAGAAAGTGGTGTGTCATCAGAG 239

QY 556 AAAAGGTGTATGATGGTATTAAAGCAGCAGCTTTAGTGAAGAGCGAGCTGAGATCT 615  
Db 240 AAAAGGTGTATGATGGTATTAAAGCAGCAGCTTTAGTGAAGAGCGATCTGATCT 299

QY 616 ACCGATGATTAGAGTGAAGCCGGATATGTTGTTCCAGGGAATTTGGGCTTTGAGT 675  
Db 300 ACTGAGGACATAGAGTGAAGCCGGATATGTTGTTCCAGGGAATTTGGGCTTTGAGT 359

QY 676 GAAGCATATGATCGTTGGGGAAGTATGTGCAGATATGCAGAGATTTTACTTAGGA 735  
Db 360 GAAGCATATGATCGTTGGGGAAGTATGTGCAGATATGTCAAGACATTTTACTTAGGA 419

QY 736 ACCAAGCTAATGACCCAGAGAGAGAGAGCTATCTGGCAATATATGTGTGGTGACAG 795  
Db 420 ACCATGCTAATGACTCCAGACAGAGAGAGCTATCTGGCAATATATGTGTGGTGACAG 479

QY 796 AGAAGGATGAGCTGTGTGATGGCCCTAATGCATCCACATAACTCCCAAGCTTTAGAT 855  
Db 480 AGAAGTATGAGCTGTGTGATGGCCCTAATGCATCCACATAACTCCCAAGCTTTAGAT 539

QY 856 AGTGGGAGACAGCGCTGGAAGATATTTTCAAGCGGCGCCATATGATATGCTTATGCT 915  
Db 540 AGTGGGAGCGCGCTGGAAGATATTTTCAAGCGGCGCCATATGATATGCTTATGCT 599

QY 916 GCTTTATCCGATAGTCTCCAGATTTCTCTGATATTCAGCCATTCCAGAGATATGAT 975  
Db 600 GCTTTATCCGATAGTCTTTCCAAATTTCTCTGATATTCAGCCATTCCAGAGATATG 659

QY 976 GAAGGAATGCGTATGGAC 993  
Db 660 GAAGGAATGCGTATGGAC 677

RESULT 5  
AW442101  
LOCUS EST311497 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA  
DEFINITION clone cLEN21G20 5', mRNA sequence.  
ACCESSION AW442101  
VERSION AW442101.1 GI:6977352  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.  
REFERENCE 1 (bases 1 to 686)  
AUTHORS Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.  
TITLE Generation of ESTs from tomato fruit tissue  
JOURNAL Unpublished (1999)  
COMMENT Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

FEATURES  
source  
1..686  
/organism="Lycopersicon esculentum"  
/cultivar="TA96"  
/db\_xref="taxon:4081"  
/clone\_lib="tomato fruit red ripe, TAMU"  
/tissue\_type="pericarp"  
/dev\_stage="red ripe (7-20 days post-breaker)"  
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Giovannoni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

BASE COUNT 204 a 114 c 182 g 186 t  
ORIGIN

Query Match 32.0%; Score 552.2; DB 10; Length 686;  
Best Local Similarity 87.9%; Pred. No. 7.3e-144;  
Matches 602; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 565 TATGATGTGTTAAAGAGCGGAGCTTTAGTGAAGAGCGAGCTGAGATCTACCGATGAT 624



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Db 661 TAAATGGAGAATCTTTATGAAGAACAA---TACTAGGGCAAGAAAGTCTTTTGATGAGCA 717
QY 1344 AGAGAAAGGTGTCA 1359
Db 718 GAGAAAGCGTGACAGA. 733

RESULT 7
BM409200
LOCUS EST383527 tomato breaker fruit Lycopersicon esculentum cDNA clone
DEFINITION cLEG47J1.5' end, mRNA sequence.
ACCESSION BM409200
VERSION BM409200.1 GI:18260830
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 682)
REFERENCE
AUTHORS Alcalá,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai
,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage. (2002)
Unpublished (2002)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
Location/Qualifiers
1..682
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone_lib="tomato breaker fruit"
/tissue_type="pericarp"
/dev_stage="breaker"
/lab_host="SOL"
/note="Vector: pBluescriptSMCadapt; Site_1: EcoRI;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
BASE COUNT 217 a 114 c 173 g 178 t
ORIGIN

Query Match 31.3%; Score 541.2; DB 13; Length 682;
Best Local Similarity 87.1%; Pred. No. 9.1e-141;
Matches 594; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 706 GCAGAGTATGCAAGACATTTTACTTAGGACCAAGCTAATGACCCAGAGAGAAGA 765
|||||
Db 1 GCAGAGTATGCAAGACGTTTACTTAGGAACTATGCTAATGACTCCCGAGAGAAGA 60
|||||

QY 766 GCTATCTGGCATATATGTGGTGCAGGAGACCGATGAGCTTTGATGCCCTAAT 825
|||||
Db 61 GCTATCTGGCAATATATGTGGTGCAGAGAACATGACTTTGATGGCCCAAC 120
|||||

QY 826 GCATCCACATACTCCGCAAGCTTTAGATAGTGGAGACCGAGCTGGAAGATATTTTC 885
|||||
Db 121 GCATCATATATTACCCGCGAGCTTAGATAGTGGGAANATAGGCTAGGAAGATTTTC 180
|||||

QY 886 AGTGGCGGCCATTTGATGCTTGTGCTTTTATCCGATACTGCTCCAGATTTCT 945
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Db 181 AATGGCGGCCATTTGACATGCTCGATGGTGGCTTTGTCCGATACAGTTTCTAATTTCCA 240
QY 946 GTTGATATTACGCATTTCAGAGATATGATTTGAAGGAATCGGTATGGACTTTGTGAAATCC 1005
|||||
Db 241 GTTGATATTACGCATTTCAGAGATATGATTTGAAGGAATCGGTATGGACTTTGAGAAATCG 300
|||||

QY 1006 AGATACAAAACITTCGATGAGCTATATCTCTATTGTACTATATTGCTGGTACTGTAGGA 1065
|||||
Db 301 AGATACAAAACITTCGACCAACTATATACCTTTATTTGTTATTGTTGCTGGTACGATGG 360
|||||

QY 1066 TTGATGAGTGTTCACCTTATGCGTATTGCACTGAATCAAGCAACAAACAGAGAGTGA 1125
|||||
Db 361 TTGATGAGTGTTCACCTTATGCGTATTGCGTATGCGCCCTGAATCAAGCAACAAACAGAGAGTGA 420
|||||

QY 1126 TATAATGCTGCTTTGGCTTTAGGGCTTGCAATCAACTAACCAATATATCTACAGAGATGA 1185
|||||
Db 421 TATAATGCTGCTTTGGCTTGCGGATCGCAATCAATTAACATACTACAGAGATGT 480
|||||

QY 1186 GGAGAGATGCCAGAGAGAGAGATATCTTGCCTCAAGATGAATAGACAGAGAGG 1245
|||||
Db 481 GGAGAGATGCCAGAGAGAGAGATCTTCTTGTGAGCAGAGAAAGCGTGACAGAAATG 540
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QY 1246 CTCTCCGAGAGACATATTTGCTGGAAGAGTCACTGATAGTGGAGAACTTTATCAAG 1305
|||||
Db 541 CTATCCGATGAGATATATTTGCTGGAAGGTGACCGATAAATGGAGAACTTTATCAAG 600
|||||

QY 1306 AAACAATTCAGAGCGGAGAGAAATTTCTTTGATGAGTCAGAGAAAGGTGTCACAGACTG 1365
|||||
Db 601 AAACAATACATAGGCGCAAGAAAGTTCTTTGATGAGCAGAGAAAGCGTGACAGAAATG 660
|||||

QY 1366 GACTGCTGCTAGTAGTGGCTG 1387
|||||
Db 661 AGCTCAGCTAGTAGATTCCTG 682

RESULT 8
AW442407
LOCUS EST311803 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
DEFINITION clone cLEN22L14 5', mRNA sequence.
ACCESSION AW442407
VERSION AW442407.1 GI:6977658
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 672)
REFERENCE
AUTHORS Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..872
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone_lib="tomato fruit red ripe, TAMU"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the

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blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

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BASE COUNT      212 a  112 c  170 g  178 t
ORIGIN

Query Match      30.8%; Score 532.8; DB 10; Length 672;
Best Local Similarity 87.1%; Pred. No. 2.1e-138;
Matches 585; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 719 AGACATTTTACTAGAACCAAGCTAATGACCCAGAGAGAGAGAGAGCTATCTGGGCAA 778
Db 1 AGACGTTTAACTTAGCACTAGCTAATGACTCCCGAGAGAGAGAGGCTATCTGGGCAA 60

QY 779 TATATGTGTGGTGCAGGAGAGGATGAGCTGTGTTGATGGCCCTAATGCATCCCAATAA 838
Db 61 TATATGTATGGTGCAGAGAGAGAGATGAACCTGTTGATGGCCCAACGCATCATATATTA 120

QY 839 CTCGCCAAGCTTTAGATAGGTGGGAGACCGCTGGAAGATATTTTCAGTGGCGGCCAT 898
Db 121 CCCCGCAGCCTTAGATAGGTGGGAAATAGCTAGAGATGTTTTCATGGCGGCCAT 180

QY 899 TTGATATGCTTGATGCTGCTTATCCGATACCTGCTCCAGATTTCTCTGTGATATTCAGC 958
Db 181 TTGACATGCTGATGCTGCTTGTTCGGATACAGTTTCACTTCCAGTTGATATTCAGC 240

QY 959 CATTGAGATATGATGATGAGAAATGCGTAGGACTTGTGGAATCCAGATACAAACTT 1018
Db 241 CATTGAGATATGATGATGAGAAATGCGTAGGACTTGTGGAATCCAGATACAAACTT 300

QY 1019 TCGATGAGCTATATCTTATTTCTTACTATGTTGCTGGTACTGTAGGATTTGATGCTTC 1078
Db 301 TCGACGAACTATACCTTTATGCTTATTTATGTTGCTGGTACGTTGGTGGTGGTTC 360

QY 1079 CAGTTATGGGTATTCACCTGAATCAAGGCAACAGCAGAGAGTGTATATATGCTGCTT 1138
Db 361 CAATTATGGGTATTCGCTGAATCAAGGCAACAGCAGAGAGCTATATATGCTGCTT 420

QY 1139 TGGCTTTAGGGCTTGCATCAATCACTAACCAATATCTCAGAGATGTAGAGAGATGCCA 1198
Db 421 TGGCTTGGGGATCCCAATCAATTAACCAATATCTCAGAGATGTAGAGAGATGCCA 480

QY 1199 GAAGAGGAGAGTATATCTGCTCAAGATGAATAGCAGCAGCGGCTCTCCGACGAAG 1258
Db 481 GAAGAGGAGAGTATCTGCTCAAGATGAATAGCAGCAGCGGCTCTCTCCGATGAAG 540

QY 1259 ACATATTTGCTGGAAGAGTGTACTGATAAGTGGAGGAATTTTATGAAGAAACAAATTCAGA 1318
Db 541 ATATATTTGCTGGAAGGTGACCGATAAATGAGAACTTTTATGAAGAAACAAATACATA 600

QY 1319 GGGCAGGAGAAATCTTTGATGAGTCAGAGAAAGGTGTCCAGAACTGGACTCTGTAGTA 1378
Db 601 GGGCAGGAAAGTCTTTGATGAGTCAGAGAAAGGTGTCCAGAACTGGACTCAGCTAGTA 660

QY 1379 GATGCGCTGCTGT 1390
Db 661 GATTCCTGCTAT 672

RESULT 9
LOCUS BE433198
DEFINITION EST399727 tomato breaker fruit; TIGR Lycopersicon esculentum cDNA
clone cLEG12N5, mRNA sequence.
ACCESSION BE433198
VERSION BE433198.1 GI:9431041
KEYWORDS EST
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 642)  
Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, I.S., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J., and Tanksley, S.D.

Generation of ESTs from tomato fruit tissue, breaker stage  
Unpublished (2000)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

#### FEATURES

Location/Qualifiers

1..642  
/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="cLEG12N5"  
/clone\_lib="tomato breaker fruit, TIGR"  
/tissue\_type="pericarp"  
/dev\_stage="breaker"  
/lab\_host="SOLR"

Generation of ESTs from tomato fruit tissue, breaker stage  
Site\_1: EcoRI;  
Site\_2: XhoI; Fruit were harvested at the breaker stage of (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp.  
194 a 103 c 167 g 178 t

#### BASE COUNT

194 a 103 c 167 g 178 t

#### ORIGIN

Query Match 30.2%; Score 522; DB 10; Length 642;  
Best Local Similarity 88.3%; Pred. No. 2.2e-135;  
Matches 567; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 660 TTTGGGCTTGTGAGTGAAGCATATGATCGTTGTGCGGAAGTATGTGCAGAGTATGCAA 719  
Db 1 TTTGGGCTTGTGAGTGAAGCATATGATGAGTGTGCGGAAGTATGTGCAGAGTATGCAA 60

QY 720 GACATTTTACTTAGAACCAAGCTAATGACCCAGAGAGAGAGAGAGTATCTTGGCAAT 779  
Db 61 GAGCTTTAACTTAGAACCTATGCTAATGACTCCCGAGAGAGAGAGGCTATCTTGGCAAT 120

QY 780 ATATGTGTGTCAGAGAGAACGGATGAGCTTGTGATGGCCCTTAATGTCATCCACATAAC 839  
Db 121 ATATGTGTGTCAGAGAGAACGGATGAGCTTGTGATGGCCCTTAATGTCATCCACATAAC 180

QY 840 TCCGCAAGCTTTAGATAGTGGGAGACCGCTGGGAAGATATTTTCAGTGGCGGCCAT 899  
Db 181 CCCGCGAGCCTTAGATAGTGGGAAATAGGCTAGAGATGTTTTCAGTGGCGGCCAT 240

QY 900 TGATATGCTGTGCTGCTTTATCCGATACCTGCTCCAGATTTCCCTGTTGATATTCAGCC 959  
Db 241 TGACATGCTGATGCTGCTTTGCTCCGATACAGTTTCTAATTCAGTGTGATATTCAGCC 300

QY 960 ATTCAGAGATATGATTGAAGGAATGCGTATGGAGTGTGTGGAATCCAGATACAAACTTT 1019  
Db 301 ATTCAGAGATATGATTGAAGGAATGCGTATGGAGTGTGTGGAATCCAGATACAAACTTT 360

QY 1020 CGATGAGCTATATCTCTATTTGTTACTATGTTGCTGCTAGTATGATGAGTGTTC 1079  
Db 361 CGACGAACCTATACCTTTATTTATTTATTTATTTGTTGCTGCTAGTATGATGAGTGTTC 420

QY 1080 AGTTATGGTATTTGACCTGGAATCAAGGCAACAGAGAGAGTGTATATATCTGCTTT 1139  
Db 421 AATTATGGTATCGCCCTTGAATCAAGGCAACAGAGAGAGCTATATATCTGCTTT 480

QY 1140 GCGTTTGGGCTTGCATAACTCAACATATCTCAGAGATGTAGGAGAGATGCCAG 1199  
Db 481 GCGTCTGGGATCGCAATCAATTAACATACTCAGAGATGTAGGAGAGATGCCAG 540

QY 1200 RAGAGGAGAGTACTTGCCTCAGATGAATTAGCACAGCAGGGCTCTCCGACGAGA 1259  
 DB 541 RAGAGGAGAGTACTTGCCTCAGATGAATTAGCACAGCAGGGCTCTCCGATGAAGA 600  
 QY 1260 CATATTTCTGGAAGAGTACTGATAGTGAGGAGAACTTTAT 1301  
 DB 601 TATATTTCTGGAAGGTTGACCGATATGAGAACTTTAT 642

RESULT 10  
 AW222027  
 LOCUS  
 DEFINITION EST298838 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA  
 clone cLEN6L15, mRNA sequence.  
 ACCESSION AW222027  
 VERSION AW222027.1 GI:5533711  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM  
 Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 1 (bases 1 to 676)  
 Alcalá, J., Vrebalov, J., White, R., Matern, A. L., Holt, I. E., Liang, F.,  
 Upton, J., Hansen, T., Craven, M. B., Bowman, C. L., Ahn, S., Ronning, C. M.,  
 Fraser, C. M., Martin, G. B., Tanksley, S. D., and Giovannoni, J.  
 Generation of ESTs from tomato fruit tissue  
 Unpublished (1999)  
 Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.

## FEATURES

source  
 1. 676  
 Location/Qualifiers  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="cLEN6L15"  
 /tissue\_type="pericarp"  
 /dev\_stage="red ripe (7-20 days post-breaker)"  
 /note="vector: plasmid SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; supplier: Giovannoni; Fruit were tagged at the  
 breaker stage (first sign of lycopene accumulation on the  
 blossom end of the fruit) and harvested 7 days  
 post-breaker (fully red-ripe), 10 days post breaker, and  
 20 days post-breaker (over-ripe). 20 day fruit which  
 showed external or internal signs of pathogenesis were  
 discarded. Fruit were cut in half and the seeds and  
 locules were discarded prior to freezing the pericarp."  
 214 a 118 c 165 g 179 t

BASE COUNT 214 a 118 c 165 g 179 t  
 ORIGIN

Query Match 29.8%; Score 515.8; DB 10; Length 676;  
 Best Local Similarity 85.5%; Pred. No. 1.2e-133;  
 Matches 574; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 808 CTTGTGTGATGGCCCAATGTCATCCACATCTCCGCAAGCTTTAGATAGTGGGAGACC 867  
 DB 2 CTTGTGTGATGGCCCAAGCATCATATATACCCCGGAGCCCTTAGATAGTGGGAAAT 61  
 QY 868 AGGCTGGAAGATPATTTCAGTGGGGCCCATTTGATGCTTGTGCTTTATCCGAT 927  
 DB 62 AGGCTAGAAGATGTTTCAATGGGGCCCATTTTGACATGCTCGATGGCTTTGTCGAT 121  
 QY 928 ACTGCTCCAGATTTCTGTTGATATTCAGCCATTTTCAGAGATATGATTGAAGAAATGCGT 987  
 DB 122 ACAGTTTCTAATTTCCAGTTGATATTCAGCCATTTTCAGAGATATGATTGAAGAAATGCGT 181

QY 988 ATGCACTTGTGGAATCCAGATACAAAACCTTCGATGAGCTATATCTCTATTGTACTAT 1047  
 DB 182 ATGCACTTGTGGAATCCAGATACAAAACCTTCGAGCAACTATACCTTTATTGTATTAT 241  
 QY 1048 GTTCTGCTACTGTAGGATTTGATGAGTTCCTCAGTTTATGGGATTTGACACCTGAATCAAG 1107  
 DB 242 GTTCTGCTAGGTTGGTTCATGAGTTCCTCAGTTTATGGGATTTGACACCTGAATCAAG 301  
 QY 1108 GCAACAACAGAGAGTGTATATAATGCTCTTGGCTTTAGGGCTTGGCAATCACTAAC 1167  
 DB 302 GCAACAACAGAGAGTGTATATAATGCTCTTGGCTTGGGATTCGCAATCACTAAC 361  
 QY 1168 AATATCTCAGAGATGTAGGAGAGATGCCAGAGAGAGAGATGATCTTGCCTCAAGAT 1227  
 DB 362 AATATCTCAGAGATGTAGGAGAGATGCCAGAGAGAGAGATGATCTTGCCTCAAGAT 421  
 QY 1228 GAATTAGCACAGGAGGCTCTCCGACGAGACATATTTGCTGGAAGAGTACTGATAG 1287  
 DB 422 GAATTAGCACAGGAGGCTCTCCGATCAAGATATATTTGCTGGAAGAGTACTGATAG 481  
 QY 1288 TGGAGGAACTTTTGAAGAAACAAATTCAGAGGGGCGAGAAATCTTTGATGAGTCAGAG 1347  
 DB 482 TGGAGAACTTTTGAAGAAACAAATACATAGGGCAAGAAATCTTTGATGAGTCAGAG 541  
 QY 1348 AAAGGTGTACAGAACTGCTGCTAGTAGTGGCTGTGTTTAAACAGCGCTGCTGTG 1407  
 DB 542 AAAGGTGTACAGAACTGCTGCTAGTAGTGGCTGTGTTTAAACAGCGCTGCTGTG 601  
 QY 1408 TATCGCAAGATTTGGGAGGAGATTGAAGCCCAACGACTACAACTTTCACAGAGGCGT 1467  
 DB 602 TACCGCAAGATTTAGATGAGATTGAAGCCCAACGACTACAACTTTCACAAAGAGCA 661  
 QY 1468 TATGTTAGCAA 1478  
 DB 662 TATGTTAGCAA 672

RESULT 11  
 BM412533  
 LOCUS  
 DEFINITION EST586860 tomato breaker fruit Lycopersicon esculentum cDNA clone  
 cLEG60I14 5' end, mRNA sequence.  
 ACCESSION BM412533  
 VERSION BM412533.1 GI:18264163  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM  
 Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 1 (bases 1 to 634)  
 Alcalá, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S. A., Tsai,  
 J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Ronning,  
 C. M., Fraser, C. M., Martin, G. B., Tanksley, S. D., and Giovannoni, J.  
 Generation of ESTs from tomato fruit tissue, breaker stage (2002)  
 Unpublished (2002)  
 Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 This clone is available through the Clemson University Genomics  
 Institute  
 Seq primer: T3.  
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 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="cLEG60I14"  
 /tissue\_type="pericarp"

FEATURES  
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 Location/Qualifiers  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="cLEG60I14"  
 /tissue\_type="pericarp"



/dev\_stage="breaker"  
/lab\_host="SOLR"  
/note="Vector: pbluescriptskmuadap; Site\_1: EcoRI;  
Site\_2: XhoI; supplier: Boyce Thompson Institute;  
sequencing: The Institute for Genomic Research. Fruit  
were harvested at the breaker stage (first sign of  
lycopene accumulation on the blossom end of fruit). Fruit  
were cut in half and the seeds and locules were discarded  
prior to freezing the pericarp."  
BASE COUNT 200 a 105 c 160 g 169 t  
ORIGIN

Query Match 28.8%; Score 498.2; DB 13; Length 634;  
Best Local Similarity 87.6%; Pred. No. 1.1e-128;  
Matches 556; Conservative 0; Mismatches 78; Indels 1; Gaps 1;  
QY 706 GCAGAGTATGCAAGACATTTTACTTAGCAACCAAGCTAATGACCCAGAGAGAGAAGA 765  
DB 1 GCAGAGTATGCAAGACGTTTAACTTAGCACTATGCTAATGACTCCCGAGAGAGAAGG 60  
QY 766 GCTATCTGGCAATATATGTGTGGTCAGGAGACGGATGAGCTTTGTATGGCCCTAAT 825  
DB 61 GCTATCTGGCAATATATGTGTGGTCAGGAGACAGATGAAGTGTGTGATGGCCCAAC 120  
QY 826 GCATCCCAATACCTCCCAAGCTTTAGATAGTGGGAGACAGCTGGAGATATTTTC 885  
DB 121 GCATCATATATACCCCGGACGCTTAGATAGTGGGAGAAATAGGCTAGAGATGTTTC 180  
QY 886 AGTGGCGGCCATTTGATATGCTTGTATGCTGCTTATCCGATACGTGTCCAGATTTCT 945  
DB 181 NATGGCGGCCATTTGACATGCTCATGCTGTGCTTTGCGATACAGTTCTAAGTTTCA 240  
QY 946 GTTGATATTCACCATTCAGAGATATGATGAAGAAATGCGGTATGAGCTTTGGAAATCC 1005  
DB 241 GTTGATATTCACCATTCAGAGATATGATGAAGAAATGCGGTATGAGCTTTGAGAAATCG 300  
QY 1006 AGATACAAACTTTTCGATGAGTATATCTTACTTACTTACTTGTGCTGGTACTAGGA 1065  
DB 301 AGATACAAACTTTTCGATGAGTATATCCCTTATTTATTTATTTATTTATTTATTTATTT 360  
QY 1066 TTGATGAGTGTTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1125  
DB 361 TTGATGAGTGTTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
QY 1126 TATATGCTGCTTTGGCTTTAGGCTTGCATTAATCAATCAATCAATCAATCAATCAAT 1185  
DB 421 TATATGCTGCTTTGGCTTTAGGCTTGCATTAATCAATCAATCAATCAATCAATCAAT 480  
QY 1186 GGAGAGATGCCAGAGAGAGATATATCTTCCCTCAAGATGATTAATAGCAGCAGGG 1245  
DB 481 GGAGAGATGCCAGAGAGAGATATATCTTCCCTCAAGATGATTAATAGCAGCAGGG 540  
QY 1246 CTCTCCGAGAGACATATTTGCTGGAAGAGTGAATGATGATGATGATGATGATGATGAT 1305  
DB 541 CTATCCGATGAGATATATTTGCTGGAAGGTTGACCGATTAATGAGATCTTTATGAG 600  
QY 1306 AAACAAATTCAGAGGCGGAGGAATTCCTTTGATGA 1340  
DB 601 AAAC-AATACATAGGGGAGGAAGTCTTTTATGA 634

RESULT 12  
B1921390  
LOCUS  
DEFINITION B1921390 599 bp mRNA linear EST 17-OCT-2001  
EST541293 tomato callus Lycopersicon esculentum cDNA clone cLEC73K6  
5' end, mRNA sequence.  
ACCESSION B1921390  
VERSION B1921390.1 GI:16217418  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;

Asteridae: euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 599)  
Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai  
J., Utterback, T., Van Aken, S., Ronning, C.M., Fraser, C.M., Martin  
G.B., Tanksley, S.D. and Giovannoni, J.  
Generation of ESTs from tomato callus tissue (2001)  
Unpublished (2001)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
This clone is available through the Clemson University Genomics  
Institute  
Seq primer: T3.  
Location/Qualifiers  
1.599  
/organism="Lycopersicon esculentum"  
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/clone\_lib="tomato callus"  
/tissue\_type="callus"  
/dev\_stage="25-40 days old"  
/lab\_host="XL1-Blue MRF"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; supplier: Boyce Thompson Institute; sequencing: The  
Institute for Genomic Research; cLEC - Cotyledons of  
seedlings 7-10 days post-germination were excised, cut at  
both ends and placed on MS medium with no selection. Mixed  
callus was harvested at 25 and 40 days and included  
undifferentiated masses. Tomato Callus EST Library"

BASE COUNT 170 a 89 c 178 g 162 t  
ORIGIN  
Query Match 28.2%; Score 487.2; DB 13; Length 599;  
Best Local Similarity 89.3%; Pred. No. 1.3e-125;  
Matches 536; Conservative 0; Mismatches 63; Indels 1; Gaps 1;  
QY 275 TTTCTCCACATTTCCAGGTCCTCGAATGGCAGCAGGATTTGGATTCCAGTCCGAGAGGAA 334  
DB 1 TTTCTCCGAATTTCCAGGTCCTCGAATGGCAGCAGGATTTGGATTCCAGTCCGAGAGGAA 60  
QY 335 ACCGCGTCTTTTATCATCCAGGTTCTAGCTCGAGATAGGAATTTGATGCTGATCCAGAT 394  
DB 61 ACCGGGTTTGGATCATCCAGTTCCCATCTCGGATAGGAATTCGATGCGAAGGAG 120  
QY 395 GAATCAAGAAAGTGGGAGACAAAGTGGAAATTTTGGCTCTTTAAATGCTGATCCAGAT 454  
DB 121 GATTCAAGAAAGTGGGAGACAAAGTGGAAATTTTGGCTCTTTAAATGCGAGATTTGAGAT 180  
QY 455 ATTCATGCTTTGGTGGATCAAGAACTGAAAGGAGACACTTTCTCTGTACACTCCAGTT 514  
DB 181 ATTCGTTTGGAGAGATCAAGAACTGAGAAATGGAGAGAGTTTCTCTGACAGCTAGT 240  
QY 515 TGGTGGCTAGCCAGCTGGAGAAATGACTGTGTATCATGAGAAAAAGGTGTATGATGTGG 574  
DB 241 TGGTGGCTAGTCCAGCTGGAGAAATGGCTGTGTATCATCAGA-AAGAAAGTGTATGAGTGG 299  
QY 575 TATTAAAGCAGCAGCTTTAGTGAAGAGCAGCTGAGATCTACCGATGATTTAGAGATGA 634  
DB 300 TATTAAAGCAGCAGCTTTAGTGAAGAGCAGCTGAGATCTACCGATGATTTAGAGATGA 359  
QY 635 AGCCGGATATTTCTTCCAGGAAATTTGGCTTTGTTGAGTGAAGCATATGATCGTGTGG 694  
DB 360 AGCCGGATATTTCTTCCGGTAAATTTGGCTTTGTTGAGTGAAGCATATGATCGTGTGG 419  
QY 695 GCGAAGTATGTCAGAGATGCAAAAGACATTTTACTTAGGAACCAAGCTAATGACCCAG 754  
DB 420 GCGAAGTATGTCAGAGATGCAAAAGACATTTTACTTAGGAACCAAGCTAATGACCCAG 479  
QY 755 AGAAGAAAGAGCTATCTCGGCAATATATGTGTGGTGCAGGAGAACGGATGAGCTTGTG 814

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Db 480 ACAGAGAGAGCTATCTGGCCATATATGTGTGGTCAGAGAACTGAAGCTTGTGTG 539
QY 815 ATGGCCCTAATGCATCCCATAACTCCGCAAGCTTTAGATAGGTGGGAGACACAGGCTGG 874
Db 540 ATGGCCCTAATGCATCACACATAAATCCACAAAGCTTTAAATAGGTGGGAGGCAAGGCTGG 599

RESULT 13
BE460889
LOCUS EST412308 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
DEFINITION EST412308 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
ACCESSION BE460889
VERSION BE460889
KEYWORDS BE460889.1 GI:9505191
SOURCE EST.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 600)
AUTHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
,S.D.
TITLE Generation of ESTs from tomato fruit tissue, breaker stage
JOURNAL Unpublished (2000)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
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/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone_lib="tomato breaker fruit, TIGR"
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/lab_host="SOLR"
/note="Vector: pBluescriptSKmCudapt; Site_1: ECOR1;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 178 a 99 c 157 g 166 t
ORIGIN
Query Match 28.1%; Score 486.4; DB 10; Length 600;
Best Local Similarity 88.2%; Pred. No. 2.2e-125; Indels 0; Gaps 0;
Matches 529; Conservative 0; Mismatches 71;
QY 650 TTCCAGGGAATTTGGCTTTTGGTGAAGCATATGCTGTGGCGAAGTATGTGCGAG 709
Db 1 TTCCGGGGAATTTGGCTTTTGGTGAAGCATATGCTGTGGCGAAGTATGTGCGAG 60
QY 710 AGTATGCAAGACATTTTACTTAGGAACCAACGTAATGACCCACAGAGAGAAAGACTA 769
Db 61 AGTATGCAAGACGCTTTAACTTAGGAACATGCTTAATGACTCCCGAGAGAAAGGCTTA 120
QY 770 TCTGGGCAATATATGTGTGGTCAGGAGACGATGCTGTGTGATGCCCTAATGCTAT 829
Db 121 TCTGGGCAATATATGTGTGGTCAGGAGACAGATGCTGTGTGATGCCCTAATGCTAT 180
QY 830 CCCCACTAATCCGCAAGCTTTTAGATAGGTGGGAGACCAAGCTTGGGAAGATATTTTCAGTG 889
Db 181 CATATATTACCCGCGAGCTTAGATAGGTGGGAAATAGGCTAGGAAGATGTTTCAATG 240

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QY 890 GCGGGCCATTTGATATGCTGTGATGCTGCTTTATCCGATACTGTCTCCAGATTTCTGTGG 949
Db 241 GCGGGCCATTTGACATGCTGCTGATGCTGCTTTGTCCGATACAGTTTCTAATTTCCAGTTG 300
QY 950 ATATTTCAGCCATTTCAGAGATATGATTGAAGGAATGCTTGGACTTGTGGAAATCCAGAT 1009
Db 301 ATATTTCAGCCATTTCAGAGATATGATTGAAGGAATGCTTGGACTTGTGGAAATCCAGAT 360
QY 1010 ACAAACCTTTTCGATGAGCTATATCTCTATTGTTACTATGTTGCTGCTAGGATTGA 1069
Db 361 ACAAACCTTTTCGAGAACTATACCTTTATTGTTATTGTTGCTGCTAGGTTGGTTGA 420
QY 1070 TGAGTGTTCAGCTTATGCTGATGCTGACCTTGAATCAAGGCCAACACAGAGAGTATATA 1129
Db 421 TGAGTGTTCAGCTTATGCTGATGCTGACCTTGAATCAAGGCCAACACAGAGAGGCTATATA 480
QY 1130 ATGCTGCTTTGGCTTTAGGCTTTCAGAACTCAACTAACCAATATCTACAGAGATGTAGGAG 1189
Db 481 ATGCTGCTTTGGCTTTCAGGAGTCCGCAATCAATTAACATACACTACAGAGATGTGGAG 540
QY 1190 AAGATGCCAGAGAGAGAGATGATATGCTTGCCTCAAGATGAATTAGCACAGGCGGCTCT 1249
Db 541 AAGATGCCAGAGAGAGAGATGATGCTTGCCTCAAGATGAATTAGCACAGGCGGCTCTAT 600

RESULT 14
BE432511
LOCUS EST399040 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
DEFINITION EST399040 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
ACCESSION BE432511
VERSION BE432511
KEYWORDS BE432511.1 GI:9430354
SOURCE EST.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 623)
AUTHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
,S.D.
TITLE Generation of ESTs from tomato fruit tissue, breaker stage
JOURNAL Unpublished (2000)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
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/dev_stage="breaker"
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/note="Vector: pBluescriptSKmCudapt; Site_1: ECOR1;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 191 a 101 c 164 g 167 t
ORIGIN
Query Match 28.0%; Score 483.4; DB 10; Length 623;
Best Local Similarity 87.2%; Pred. No. 1.6e-124; Indels 4; Gaps 1;
Matches 543; Conservative 0; Mismatches 76;

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